EFS ID: 7262650

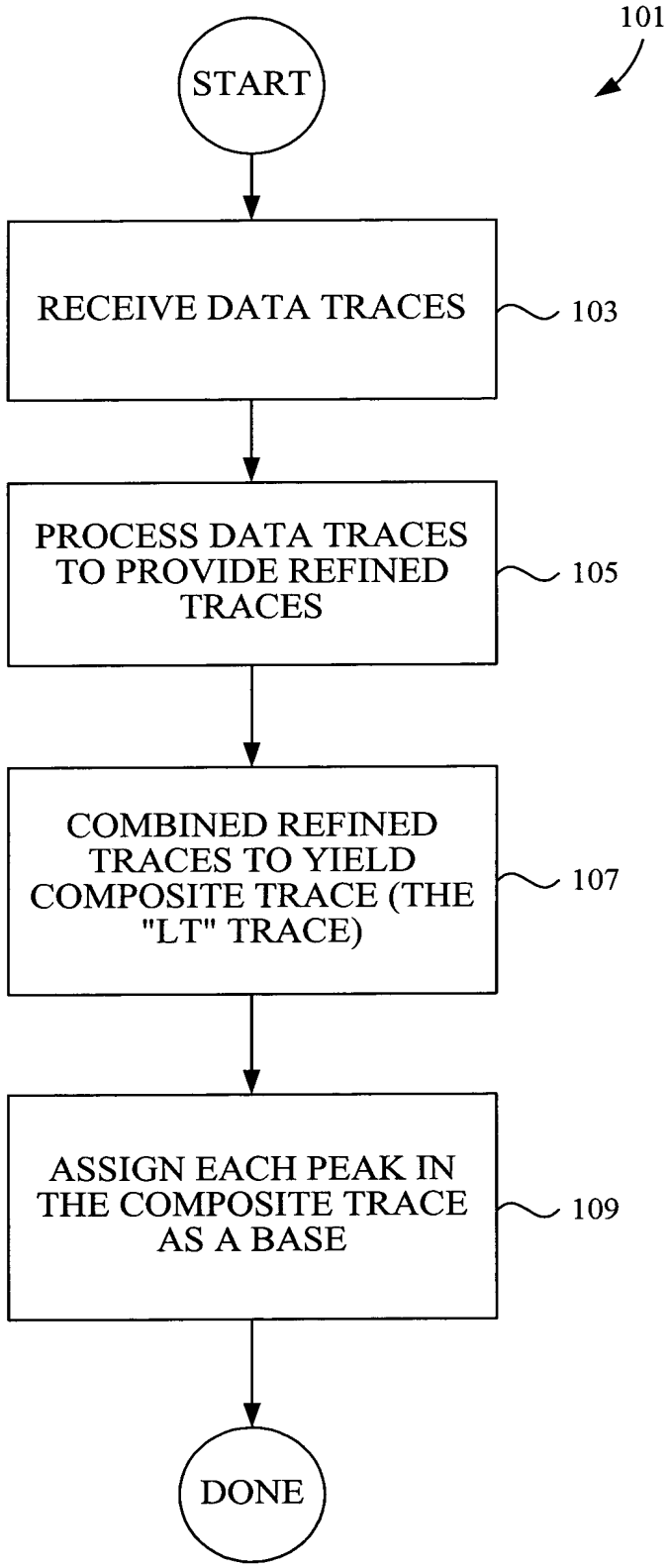


FIG. 1

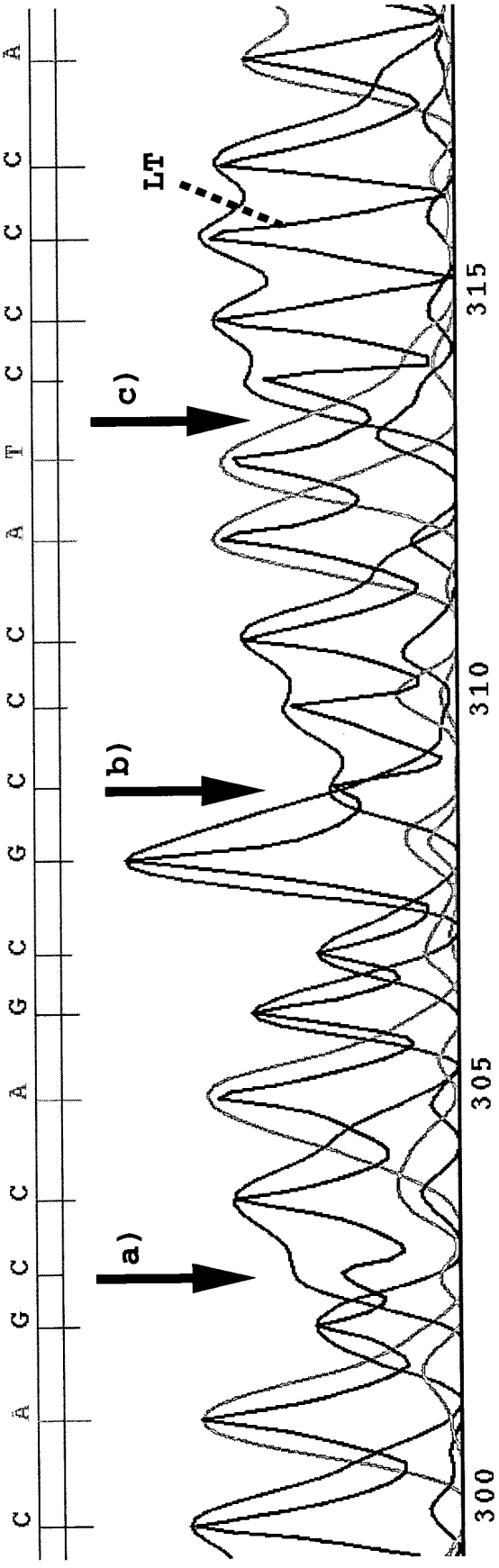


FIG. 2

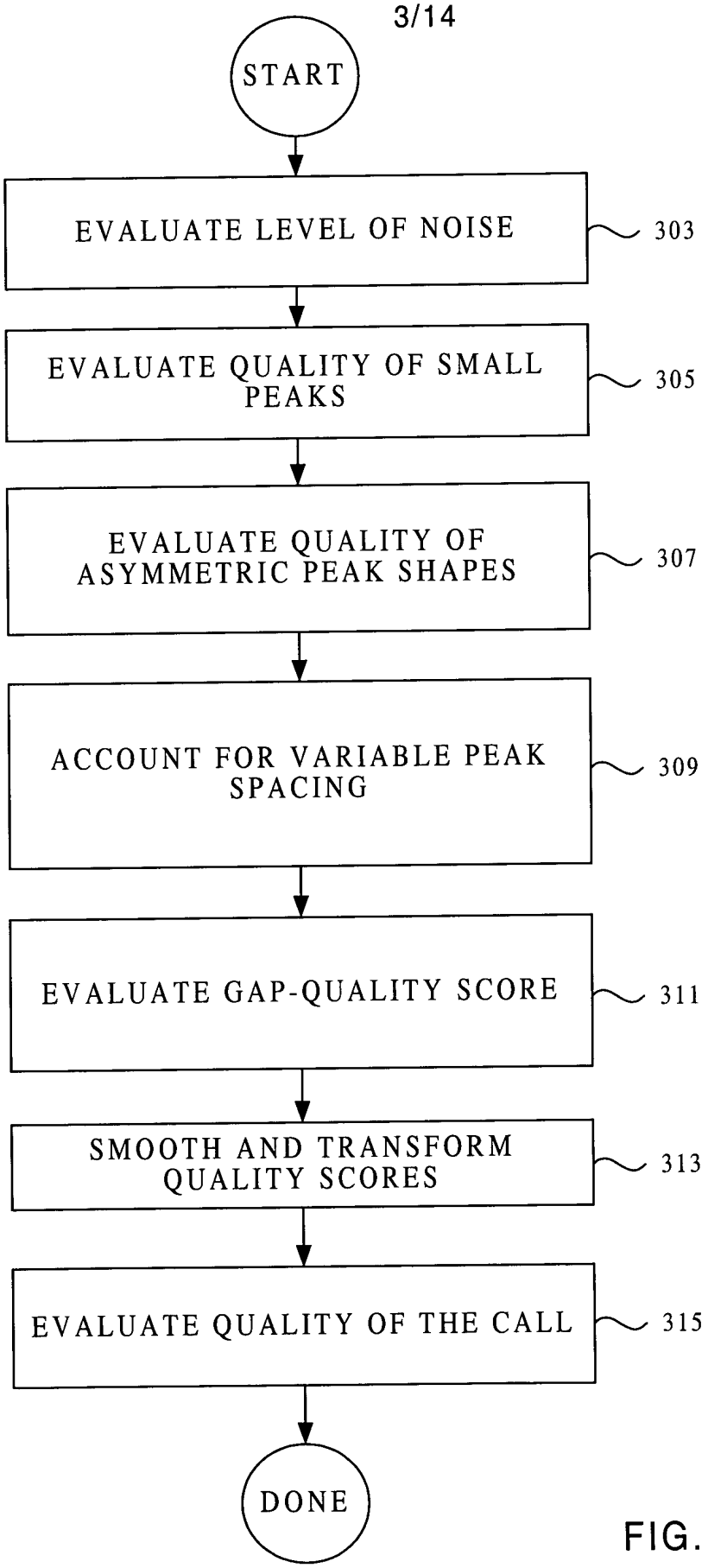
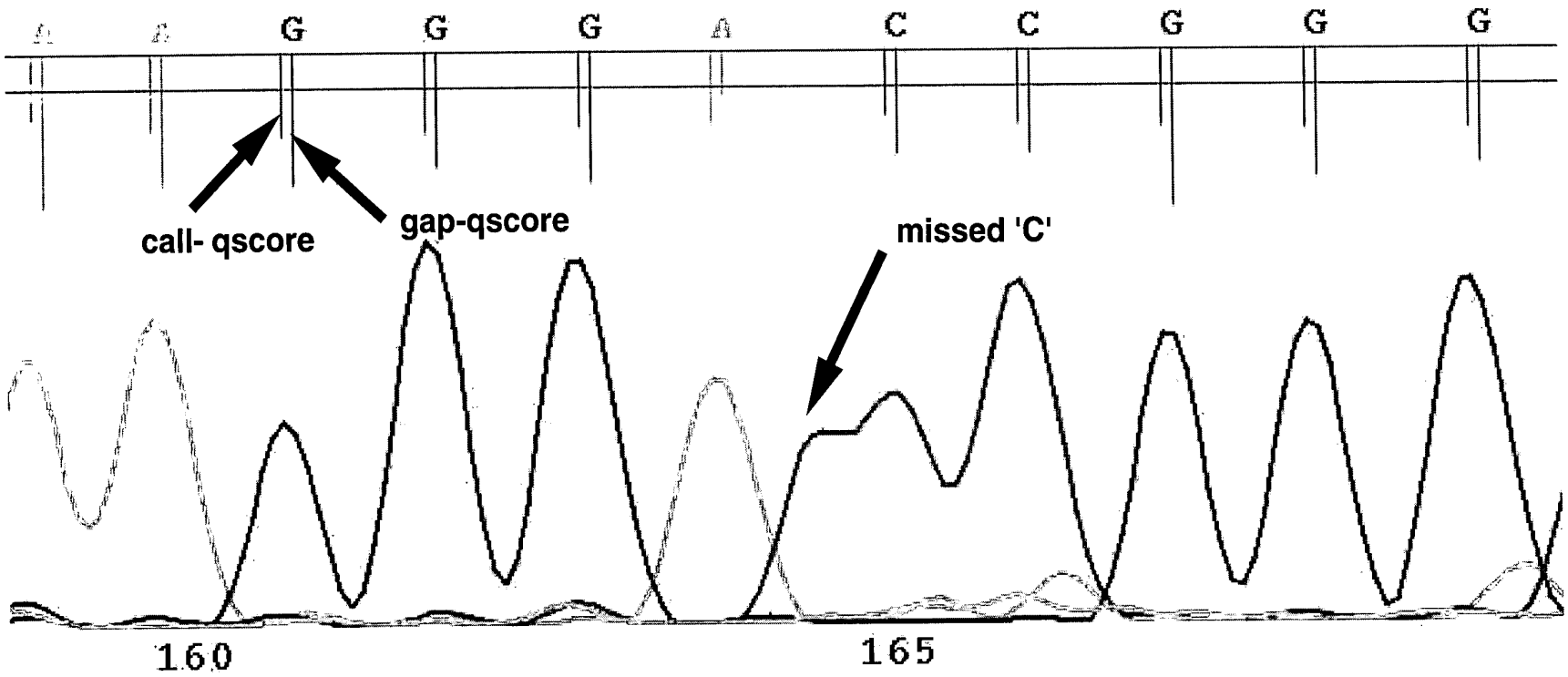


FIG. 3

EP0F80 T2E2650



AAGGGA**CCC**GGG true sequence

alignment alternatives:
AACGGA**CC**-GGG
AACGGA**C**-**C**GGG
AACGGA-**CC**GGG correct alignment

FIG. 4

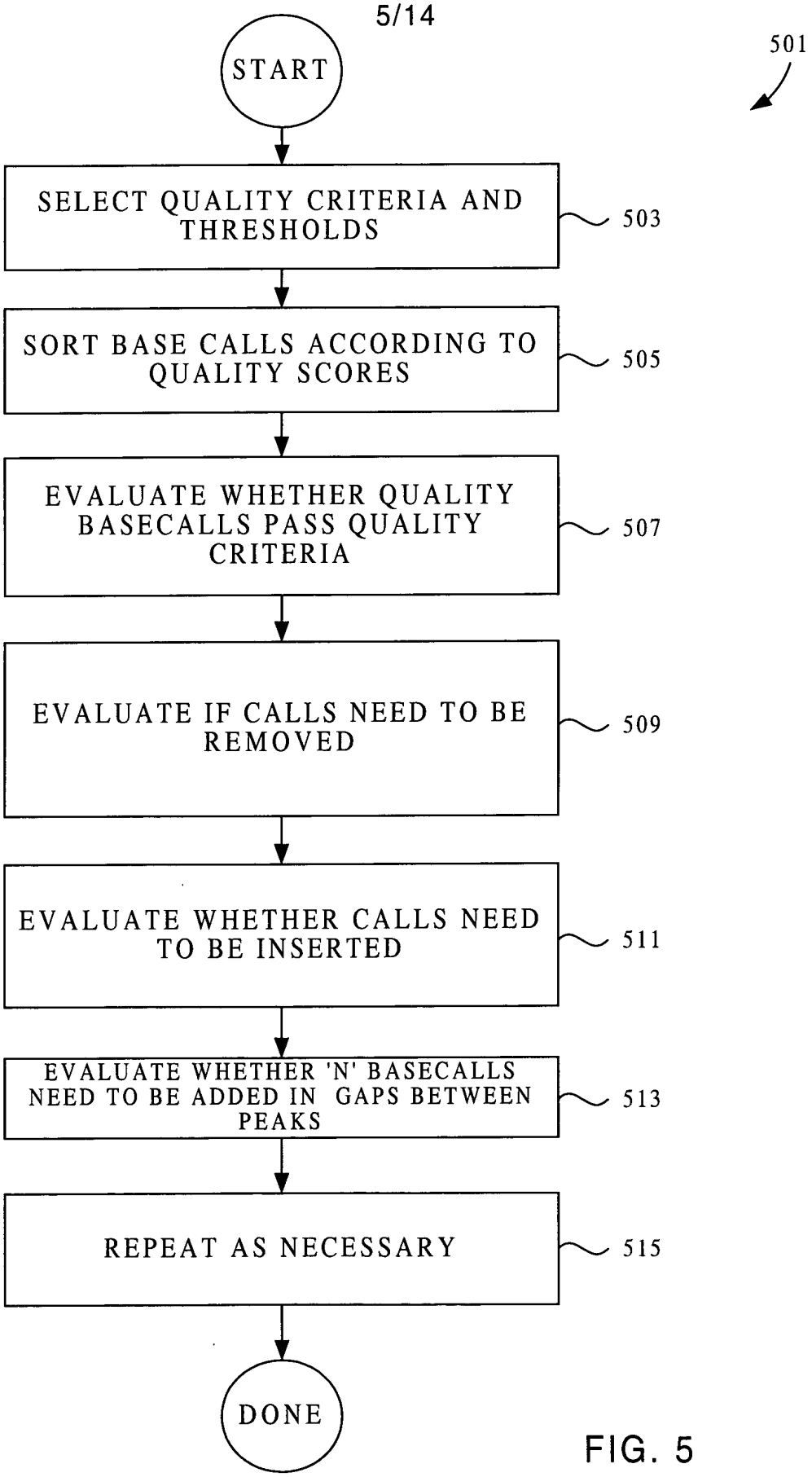


FIG. 5

EOOTBOD: WO 2004/025568

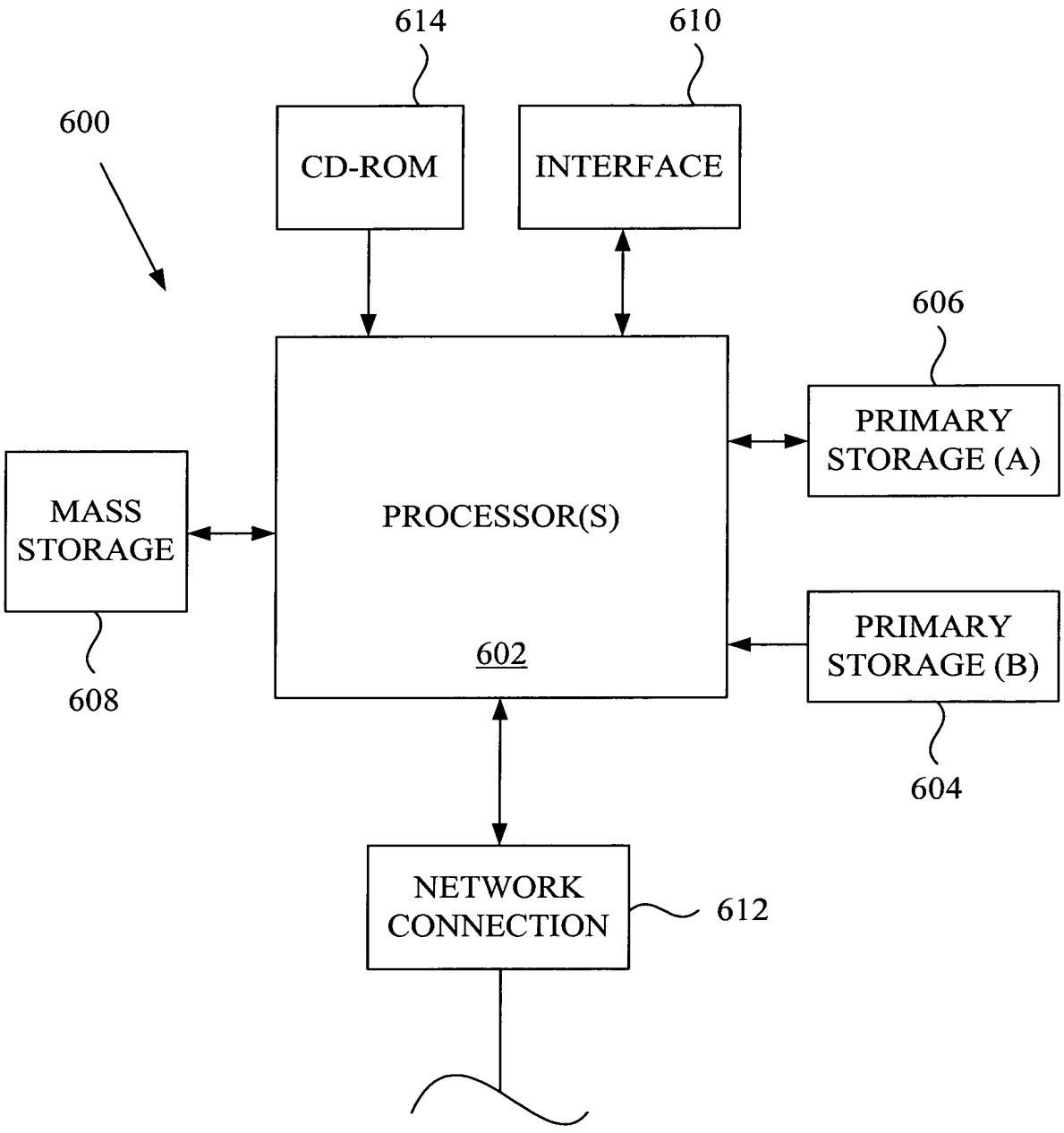

614
610
600
CD-ROM
INTERFACE
606
PRIMARY STORAGE (A)
MASS STORAGE
PROCESSOR(S)
602
PRIMARY STORAGE (B)
608
604
NETWORK CONNECTION
612

FIG. 6

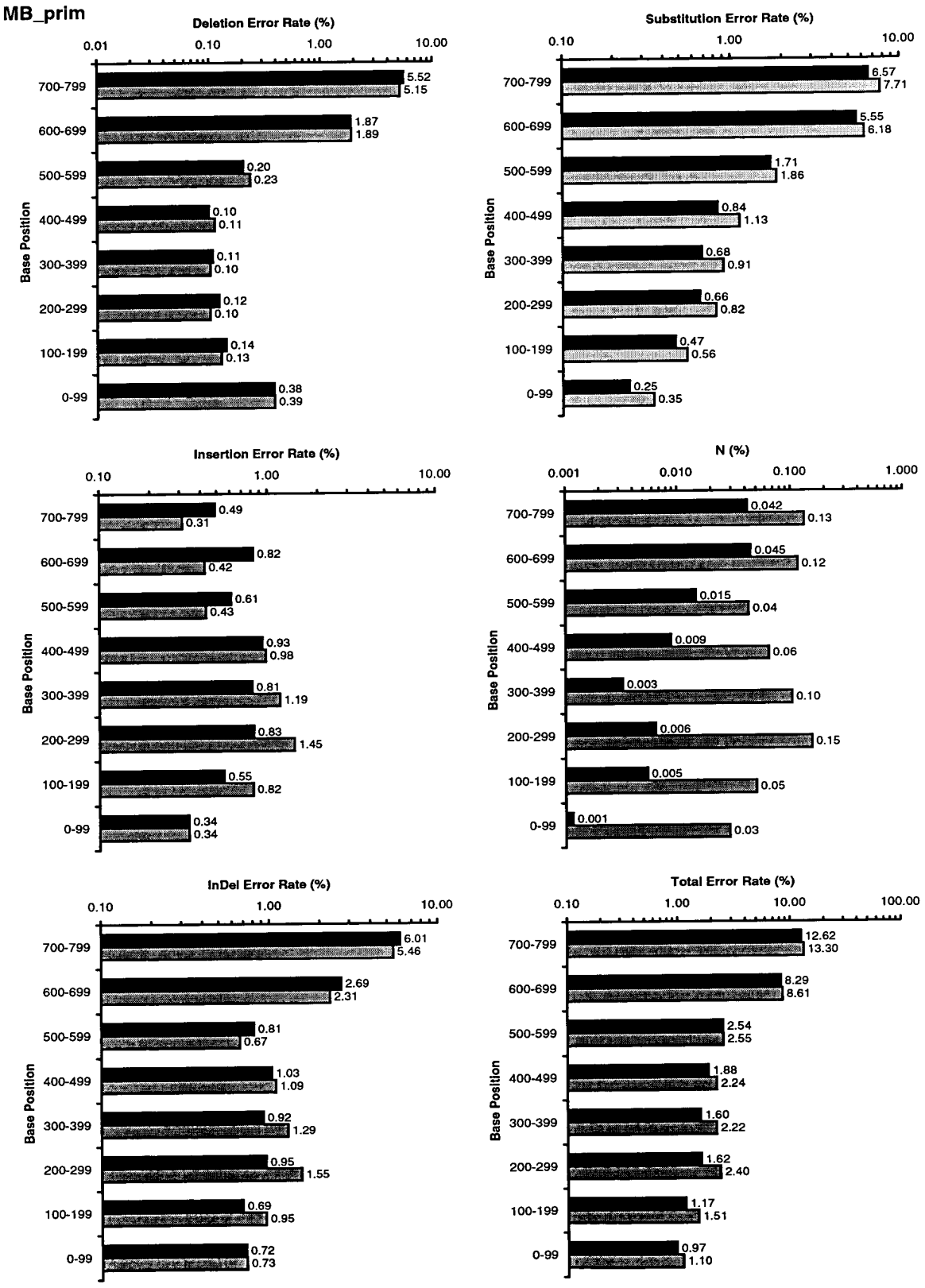

MB_prim
Deletion Error Rate (%)
0.01
0.10
1.00
10.00
Base Position
700-799
600-699
500-599
400-499
300-399
200-299
100-199
0-99
5.52
5.15
1.87
1.89
0.20
0.23
0.10
0.11
0.11
0.10
0.12
0.10
0.14
0.13
0.38
0.39
Substitution Error Rate (%)
0.10
1.00
10.00
6.57
7.71
5.55
6.18
1.71
1.86
0.84
1.13
0.68
0.91
0.66
0.82
0.47
0.56
0.25
0.35
Insertion Error Rate (%)
0.49
0.31
0.82
0.42
0.61
0.43
0.93
0.98
0.81
1.19
0.83
1.45
0.55
0.82
0.34
0.34
N (%)
0.001
0.010
0.100
1.000
0.042
0.13
0.045
0.12
0.015
0.04
0.009
0.06
0.003
0.10
0.006
0.15
0.005
0.05
0.001
0.03
InDel Error Rate (%)
6.01
5.46
2.69
2.31
0.81
0.67
1.03
1.09
0.92
1.29
0.95
1.55
0.69
0.95
0.72
0.73
Total Error Rate (%)
100.00
12.62
13.30
8.29
8.61
2.54
2.55
1.88
2.24
1.60
2.22
1.62
2.40
1.17
1.51
0.97
1.10

FIG. 7A

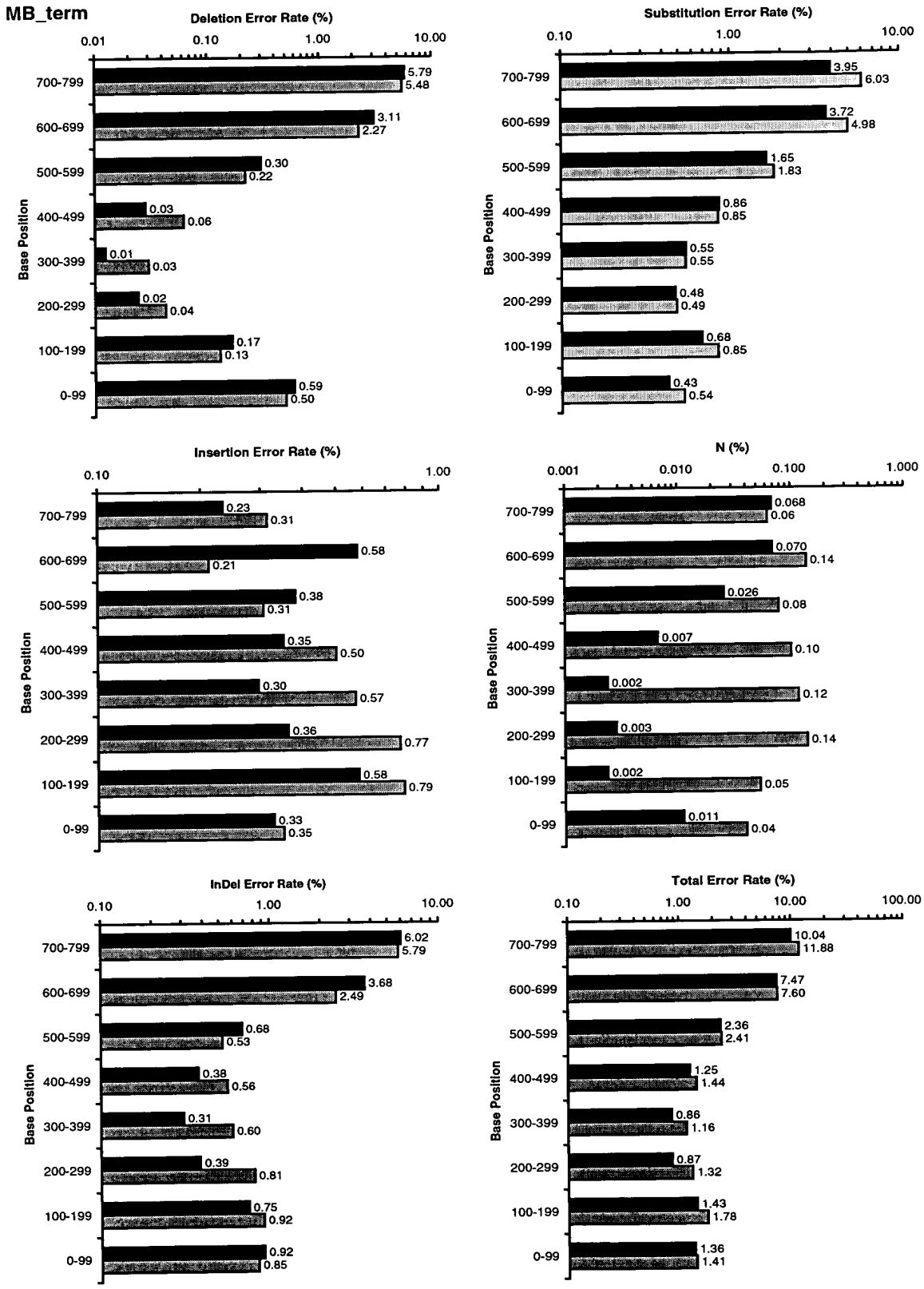

MB_term
Deletion Error Rate (%)
0.01
0.10
1.00
10.00
Base Position
700-799
600-699
500-599
400-499
300-399
200-299
100-199
0-99
5.79
5.48
3.11
2.27
0.30
0.22
0.03
0.06
0.01
0.03
0.02
0.04
0.17
0.13
0.59
0.50
Substitution Error Rate (%)
0.10
1.00
10.00
3.95
6.03
3.72
4.98
1.65
1.83
0.86
0.85
0.55
0.55
0.48
0.49
0.68
0.85
0.43
0.54
Insertion Error Rate (%)
0.10
1.00
0.23
0.31
0.58
0.21
0.38
0.31
0.35
0.50
0.30
0.57
0.36
0.77
0.58
0.79
0.33
0.35
N (%)
0.001
0.010
0.100
1.000
0.068
0.06
0.070
0.14
0.026
0.08
0.007
0.10
0.002
0.12
0.003
0.14
0.002
0.05
0.011
0.04
InDel Error Rate (%)
0.10
1.00
10.00
6.02
5.79
3.68
2.49
0.68
0.53
0.38
0.56
0.31
0.60
0.39
0.81
0.75
0.92
0.92
0.85
Total Error Rate (%)
0.10
1.00
10.00
100.00
10.04
11.88
7.47
7.60
2.36
2.41
1.25
1.44
0.86
1.16
0.87
1.32
1.43
1.78
1.36
1.41

FIG. 7B

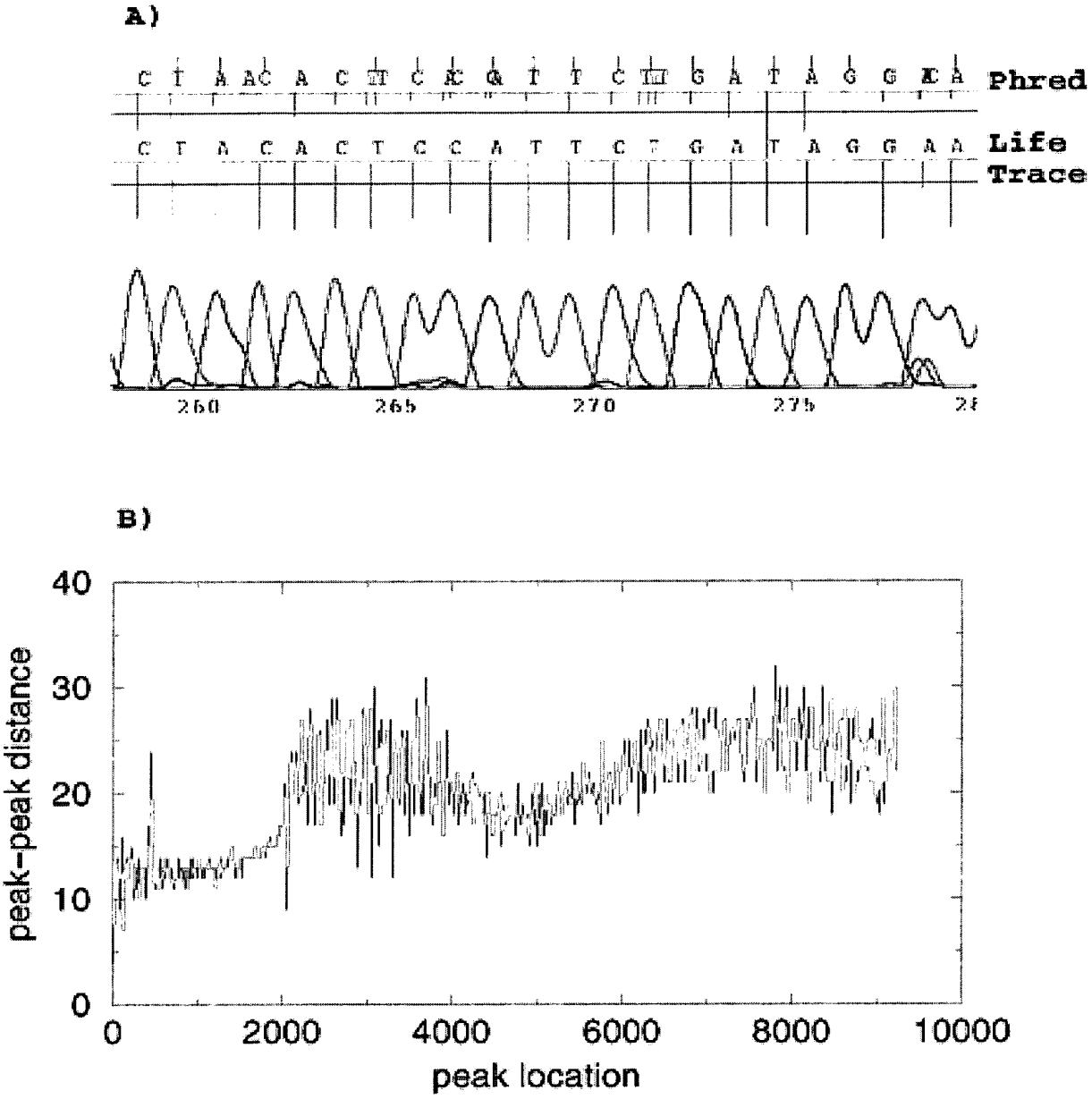

A)
Phred
Life
Trace
260
265
270
275
B)
peak-peak distance
peak location
0
10
20
30
40
0
2000
4000
6000
8000
10000

FIG. 8

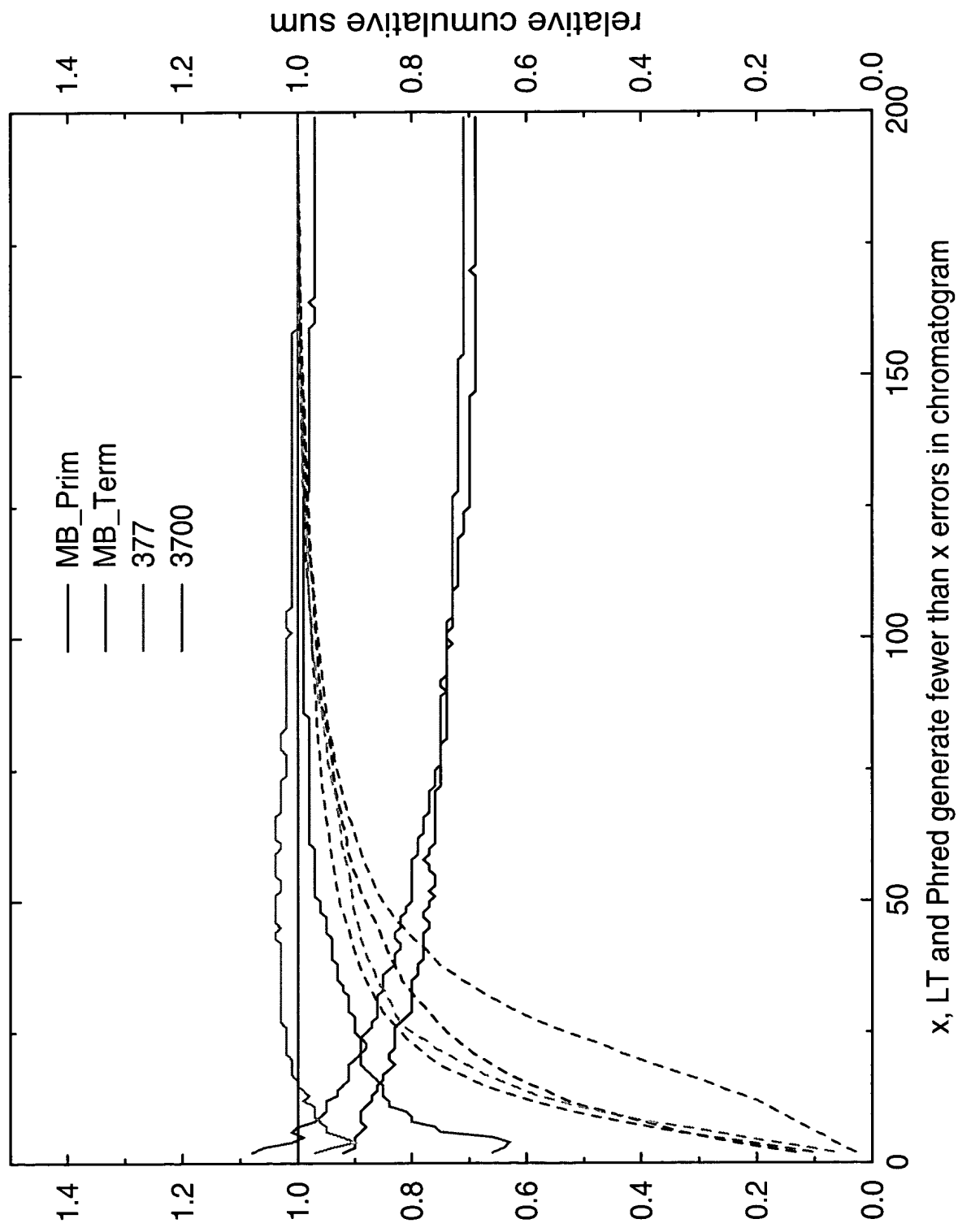

LT/Phred errors in chromatograms
relative cumulative sum
x, LT and Phred generate fewer than x errors in chromatogram
MB_Prim
MB_Term
377
3700
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
50
100
150
200

FIG. 9

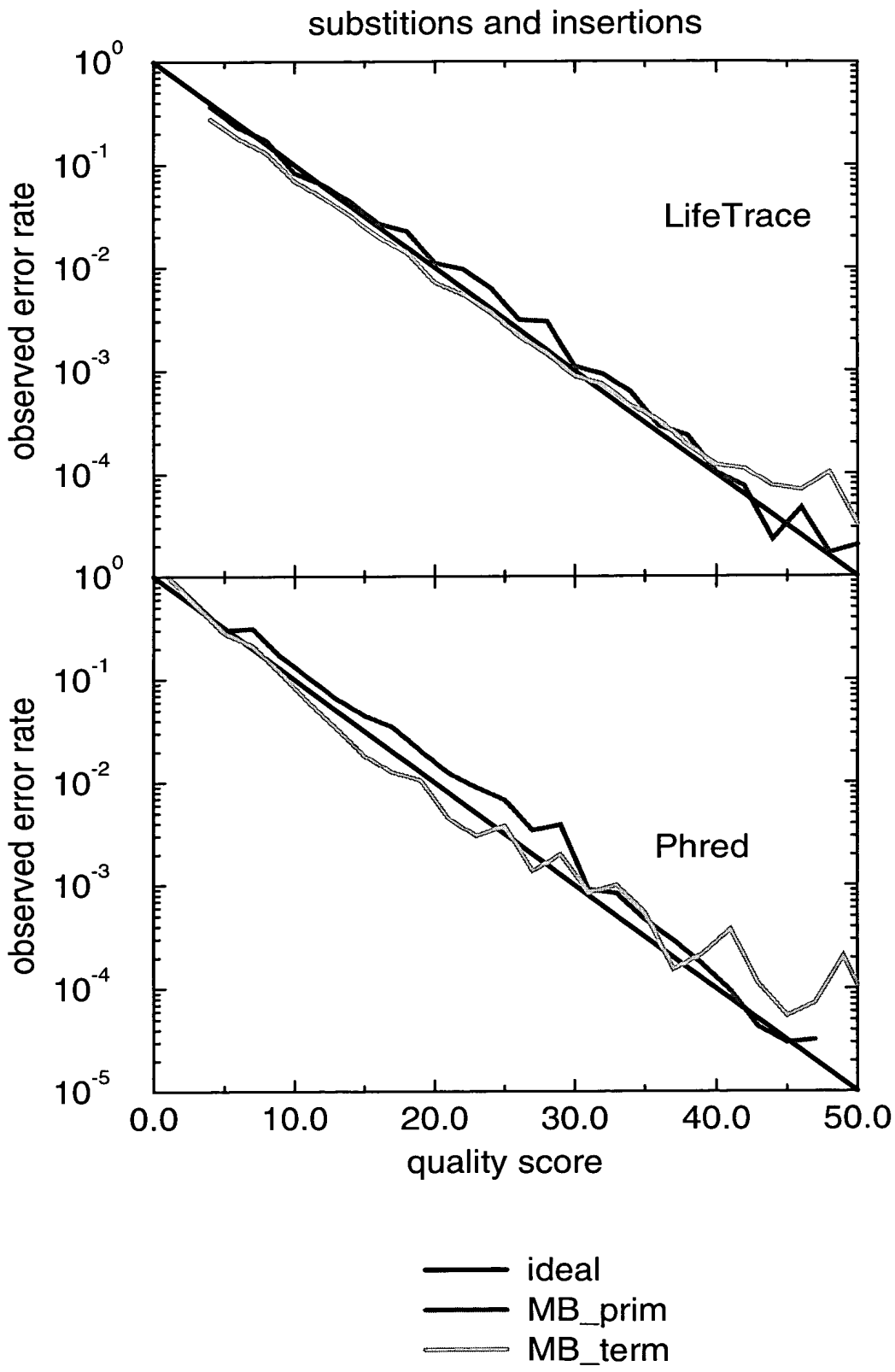

substitions and insertions
observed error rate
LifeTrace
Phred
quality score
0.0
10.0
20.0
30.0
40.0
50.0
ideal
MB_prim
MB_term

FIG. 10

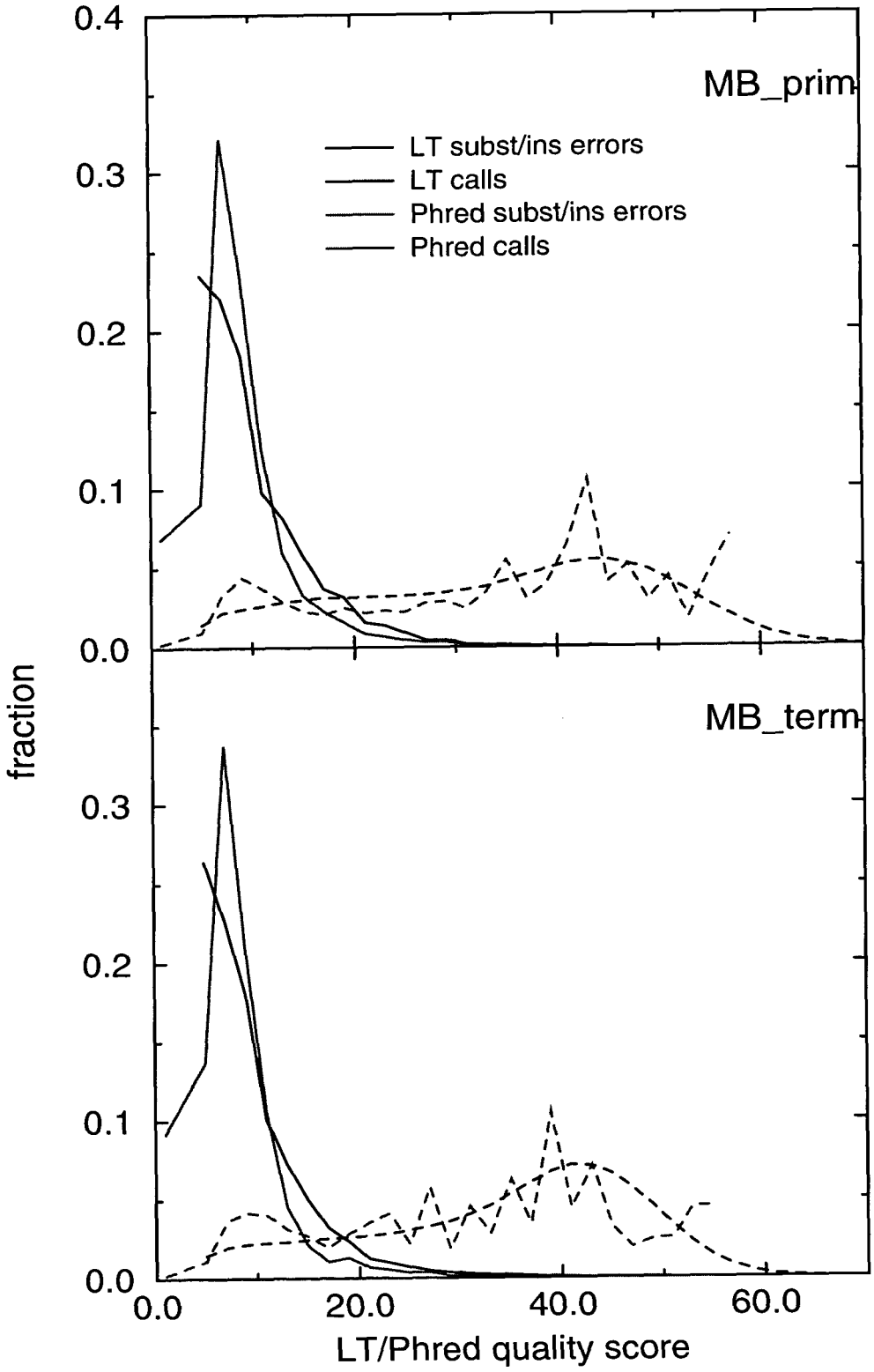

0.4
0.3
0.2
0.1
0.0
MB_prim
LT subst/ins errors
LT calls
Phred subst/ins errors
Phred calls
fraction
MB_term
0.3
0.2
0.1
0.0
0.0
20.0
40.0
60.0
LT/Phred quality score

FIG. 11

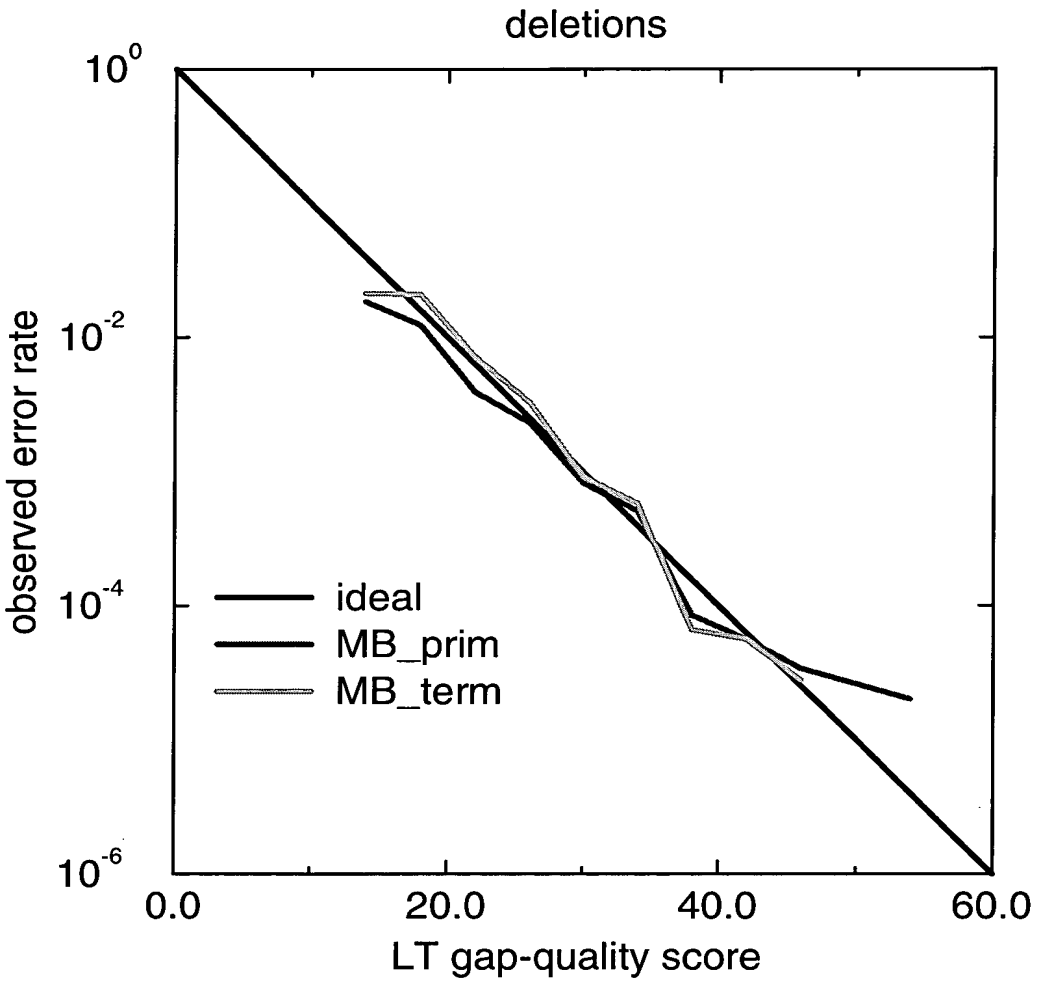

deletions
observed error rate
10^{0}
10^{-2}
10^{-4}
10^{-6}
ideal
MB_prim
MB_term
0.0
20.0
40.0
60.0
LT gap-quality score

FIG. 12

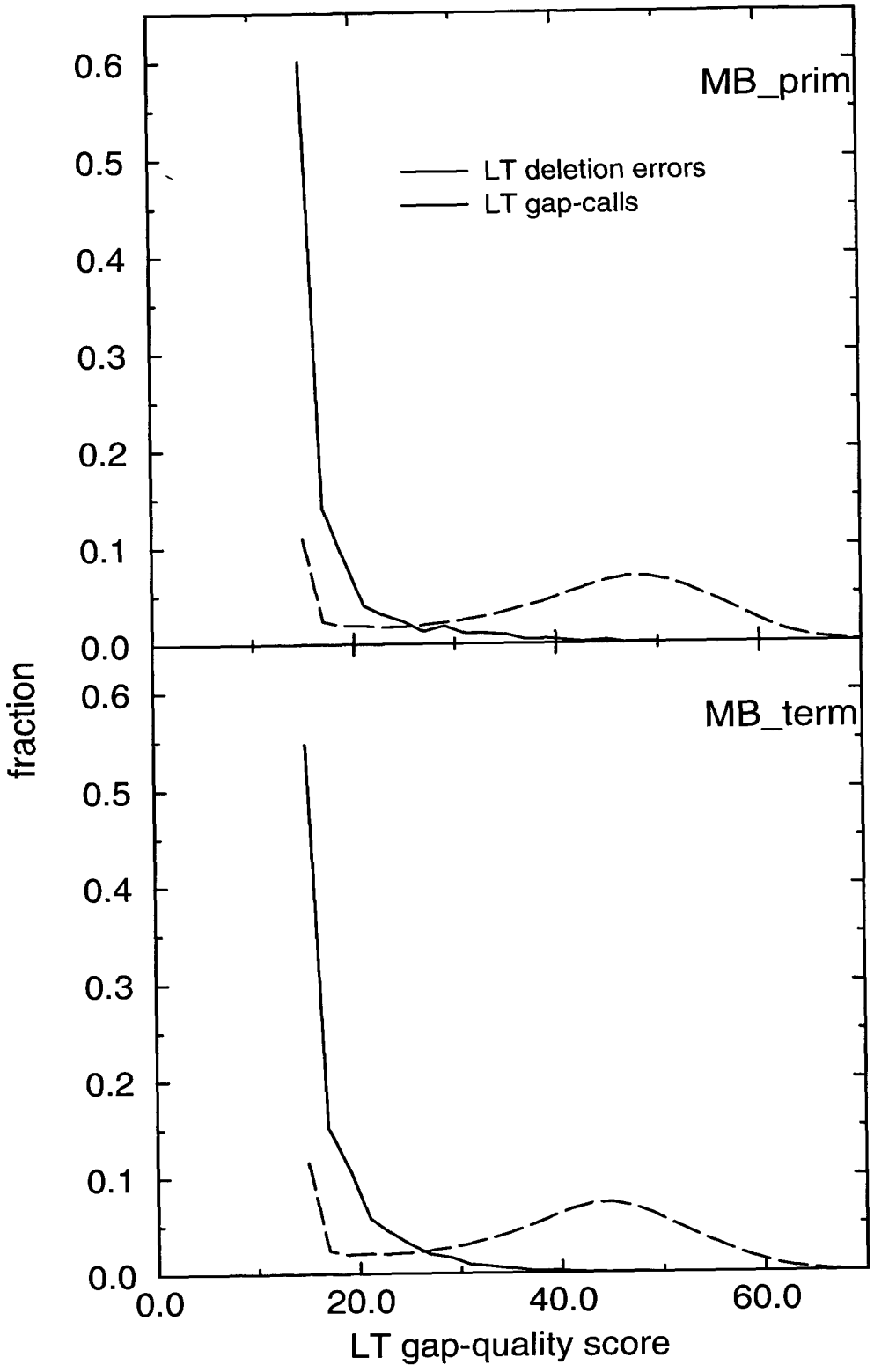

MB_prim
LT deletion errors
LT gap-calls
MB_term
fraction
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
20.0
40.0
60.0
LT gap-quality score

FIG. 13